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 M I S S I O N E R Y  
 (TM)  
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Msrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 28 20:25:28 1999, MasPar time 603.24 Seconds

Tabular output not generated. 1002.380 Million cell updates/sec

Title: >US-09-327-230-1  
 Description: (1-2822) from US09327230.seq  
 Perfect Score: 2822  
 N.A. Sequence: 1 gcaacgcacacagcagca.....ttccagtttggttcg 2822  
 Comp: cgttcgctgtctgcgt.....aagttcaacccaagccc

Scoring table: TABLE default  
 Gap 6

Mmatch STD: Dbase 0; Query 0

Searched: 271905 segs, 107135622 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: n-geneseg35  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19 20:part20 21:part21 22:part22 23:part23  
 24:part24 25:part25 26:part26 27:part27 28:part28  
 29:part29 30:part30 31:part31 32:part32 33:part33  
 34:part34 35:part35 36:part36 37:part37 38:part38  
 39:part39 40:part40 41:part41 42:part42 43:part43  
 44:part44 45:part45 46:part46 47:part47 48:part48  
 49:part49 50:part50 51:part51 52:part52 53:part53  
 54:part54 55:part55 56:part56 57:part57 58:part58  
 59:part59 60:part60

Statistics: Mean 9.803; Variance 6.092; scale 1.609

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2822	100.0	2822	51	V57302	Maize cell death supp
2	49	1.7	204	1	N81164	Base substituted E.co
3	44	1.6	91	9	O51746	Oligonucleotide probe
4	42	1.5	91	9	O51746	Oligonucleotide probe
5	42	1.5	204	1	N81164	Base substituted E.co
6	33	1.2	91	46	V44650	Mammalian DNA replica
7	34	1.2	91	46	V44650	Mammalian DNA replica
8	34	1.2	114	12	O70467	Generic DNA sequence
9	33	1.2	172	32	T76363	Human Interleukin 8 a

10	32	1.1	114	12	O70465	Generic DNA sequence
11	32	1.1	114	12	O70468	Generic DNA sequence
12	31	1.1	114	12	O70469	Generic DNA sequence
13	31	1.1	114	12	O70470	Generic DNA sequence
14	30	1.1	114	12	O70465	Generic DNA sequence
15	30	1.1	114	12	O70469	Generic DNA sequence
16	31	1.1	172	32	T76363	Human Interleukin 8 a
17	30	1.1	178	32	T76405	Human endothelin-1 an
18	27	1.0	67	24	T14322	Primer used in the la
19	29	1.0	114	12	O70472	Generic DNA sequence
20	29	1.0	114	12	O70466	Generic DNA sequence
21	28	1.0	114	12	O70471	Generic DNA sequence
22	29	1.0	114	12	O70470	Generic DNA sequence
23	29	1.0	114	12	O70466	Generic DNA sequence
24	29	1.0	114	12	O70467	Generic DNA sequence
25	29	1.0	114	12	O70468	Generic DNA sequence
26	27	1.0	190	32	T76452	Chymase antisense oli
27	29	1.0	200	32	T76398	Human leukotriene C4
28	27	1.0	250	32	T76438	Substance P antisense
29	27	1.0	657	7	O43519	Degenerate PMV reduct
30	29	1.0	2822	51	V57302	Maize cell death supp
31	26	0.9	67	24	T14322	Primer used in the la
32	26	0.9	68	34	T73397	Oligonucleotide tag c
33	26	0.9	68	32	T63255	Messenger RNA primer
34	26	0.9	70	24	T14325	Conjugate formed by 1
35	25	0.9	74	21	T13613	DC43 TSNR library gen
36	26	0.9	78	59	V82092	DBY746 Yeast cell pol
37	25	0.9	81	21	T13611	DC43 TSNR library gen
38	25	0.9	114	12	O70473	Generic DNA sequence
39	26	0.9	114	12	O70472	Generic DNA sequence
40	26	0.9	130	32	T76152	Human vascular cell a
41	25	0.9	178	32	T76405	Human endothelin-1 an
42	25	0.9	390	30	T67438	H. pylori secreted or
43	25	0.9	393	30	T67919	H. pylori secreted or
44	25	0.9	592	16	O85520	DNA probe 26 detects

#### ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
1	V57302	100.0	2822	51	V57302	Maize cell death supp	0.00e+00
2	V57302	49	1.7	204	1	N81164	Base substituted E.co
3	V57302	44	1.6	91	9	O51746	Oligonucleotide probe
4	V57302	42	1.5	91	9	O51746	Oligonucleotide probe
5	V57302	42	1.5	204	1	N81164	Base substituted E.co
6	V57302	33	1.2	91	46	V44650	Mammalian DNA replica
7	V57302	34	1.2	91	46	V44650	Mammalian DNA replica
8	V57302	34	1.2	114	12	O70467	Generic DNA sequence
9	V57302	33	1.2	172	32	T76363	Human Interleukin 8 a

OS Zea mays.  
 PN WO9839422-A1.  
 PD 11-SEP-1998.  
 PF 03-MAR-1998; U04040.  
 PR 04-MAR-1997; US-810009.  
 PA (PRON) PRONEER HI-BRED INT INC.  
 PI (DMOR) UNIV MISSOURI.  
 PI Br199s SP, Gray J, Gurmukh JS;  
 DR WPI: 98-506354/43.  
 PT New isolated plant cell death suppressing gene - used for e.g.  
 PT activating disease resistance, enhancing transformation efficiency,  
 PT engineering herbicide resistance or targeting cell ablations  
 PS Claim 38; Page 51-53; 95pp; English.  
 CC This nucleotide sequence comprises the promoter region of the  
 CC maize leaf spot-1 (lsl1) gene (see V57301 and V57303). The lsl1  
 CC gene encodes a novel maize protein (see W79001) which inhibits the  
 CC spread of cell death from wounding or internal stresses that occur  
 CC during photosynthesis. The invention relates to methods and  
 CC compositions for suppressing cell death and controlling disease  
 CC resistance in plants. The compositions, cell death suppressing  
 CC lsl1 protein and nucleic acids are useful for activating disease  
 CC resistance, enhancing cell transformation efficiency, engineering  
 CC herbicide resistance and genetically targeting cell ablations.  
 CC Novel promoter sequences are provided for the expression of genes  
 CC in plants. A chimeric gene comprising the promoter operably  
 CC linked with a heterologous coding sequence is claimed, as are a

D	b	1	gcaacgcacaaagcagcagcgatgctcttcgcgggctcagtaacctcactcaacagg	60
Q	y	1	gcaacgcacaaagcagcagcgatgctcttcgcgggctcagtaacctcactcaacagg	60
D	b	61	ctatcgcttaagtttttttggtccaacatacacaactctgtgtgtcctaagttaacaaaa	120
Q	y	61	ctatcgcttaagtttttttggtccaacatacacaactctgtgtgtcctaagttaacaaaa	120
D	b	121	aaattcaacgcctccacacaaacattacatagatctcaaaagtagacataccaaccttg	180
Q	y	121	aaattcaacgcctccacacaaacattacatagatctcaaaagtagacataccaaccttg	180
D	b	181	gaggaacttgcacgcgtcagagaacacctactcactcgtcactcgtcctacccgagacag	240
Q	y	181	gaggaacttgcacgcgtcagagaacacctactcactcgtcactcgtcctacccgagacag	240
D	b	241	agggaatacacacagacagacacgtgtgtgactgtgtgtgaaaatgacaaggaaggttag	300
Q	y	241	agggaatacacacagacagacacgtgtgtgactgtgtgtgaaaatgacaaggaaggttag	300
D	b	301	taataagcaagcatatgtatgagcgtcacaagtacaacatgatatgcctgcctcttagac	360
Q	y	301	taataagcaagcatatgtatgagcgtcacaagtacaacatgatatgcctgcctcttagac	360
D	b	361	cttcaatgatgaaataaaaaactatataagtgaaagtgaacaacatgcgttatgtataac	420
Q	y	361	cttcaatgatgaaataaaaaactatataagtgaaagtgaacaacatgcgttatgtataac	420
D	b	421	tagcagactatgtgattgaaagaattccaattacaagaacaaagaatagactgcggggc	480
Q	y	421	tagcagactatgtgattgaaagaattccaattacaagaacaaagaatagactgcggggc	480
D	b	481	agcaacacaactaactaaatgctccaaaatgctcagatgaaagggctcgagacatgcac	540
Q	y	481	agcaacacaactaactaaatgctccaaaatgctcagatgaaagggctcgagacatgcac	540
D	b	541	gacatgatabatgcctagtctggggcgtcttcgcgtcgggctttaagaataagaaacttgata	600
Q	y	541	gacatgatabatgcctagtctggggcgtcttcgcgtcgggctttaagaataagaaacttgata	600
D	b	601	tggactaatgctgctcaattttgtttgagcgtcagcgccctagcatgctcaactaagaagt	660
Q	y	601	tggactaatgctgctcaattttgtttgagcgtcagcgccctagcatgctcaactaagaagt	660
D	b	661	taatttggcttcaattttttgttcgacgcgctggcgcaacatctcttgcgtcagtaggtt	720
Q	y	661	taatttggcttcaattttttgttcgacgcgctggcgcaacatctcttgcgtcagtaggtt	720
D	b	721	acattttagtaccactcctctctgtctcaaaagaagacatactcccatctttttaaatgctc	780
Q	y	721	acattttagtaccactcctctctgtctcaaaagaagacatactcccatctttttaaatgctc	780
D	b	781	ttgctttttggaagcgacatctctttaaaactctgacccaactatataaaagtaactctga	840
Q	y	781	ttgctttttggaagcgacatctctttaaaactctgacccaactatataaaagtaactctga	840
D	b	841	tacatgataagtttaataaataataataaactatatttttggtaagcttagtcaact	900
Q	y	841	tacatgataagtttaataaataataataaactatatttttggtaagcttagtcaact	900
D	b	901	taagaagctttgacgtcgcacatagttgttttaacaaggtgtgtgtcattgctgtct	960
Q	y	901	taagaagctttgacgtcgcacatagttgttttaacaaggtgtgtgtcattgctgtct	960

[illegible]



Query Match	1.5%;	Score 42;	DB 9;	Length 91;
Best Local Similarity	18.1%;	Pred. No. 4.74e-09;		
Matches	13;	Conservative 44;	Mismatches 15;	Indels 0;
			Gaps	0;

RESULT	5
ID	N81164 standard; DNA; 204 BP.

DT 08-NOV1990 (first entry)  
DE Base substituted E.coli beta-galactosidase alpha-fragment.  
KM E.coli beta galactosidase alpha-fragment; base substitutions; ss  
OS Escherichia coli.

Key	Value
location	Qualifiers
feature	19..69
tag	a
function	multiple cloning site
primer_bind	187..204
tag	b

PD 05-MAY-1988.  
PF 30-MAR-1988; 105163.  
PR 03-APR-1987; US-034819.  
PA (SUSO) SUOMEN SOKERI OY.  
PI Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T,  
DR WPT; 88-27992//40.

PT by prepn of single stranded template, annealing a primer, elongation  
PT misincorporation, completion of molecules and screening.  
PS disclosure; p; English.

CC Random point mutations were introduced into the alpha fragment of  
CC beta-galactosidase. The wild type sequence was obtained  
CC from *E. coli* strain W3103.  
CC The alpha fragment was hybridised to a DNA probe containing  
CC the sequence of the alpha fragment of beta-galactosidase.  
CC The alpha fragment was hybridised to a DNA probe containing  
CC the sequence of the alpha fragment of beta-galactosidase.

CC it to generate a popn of DNA molecules which terminate at all  
CC possible nucleotide positions within a specified region. The  
CC variable 3' ends generated in this way are used as primers for  
CC reverse transcriptase. Nucleotides are misincorporated by the  
CC transcriptase and the molecules are completed to forms that can be  
CC amplified and then expressed in a suitable host-vector system.

CC	The sequence covers all 1/6 drift base substitutions, most of which occurred singularly in any given mutant.
CC	See also P80575.
CC	Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;
CC	Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match	1.5%;	Score 42;	DB 1;	Length 204;
Best Local Similarity	15.1%;	Pred. No. 4.74e-09;		
Matches	14;	Conservative	49;	Mismatches 29;
			Indels	1;
			Gaps	1;

Dd 91 thyrirmbnvryrnrsdaawycyrrsvkydcocynachdhdybbbyvnmhmnn 150  
::: :: :: :: ||| : : ::||| |::::: :::: :::  
Cp 2383 ttctcaaacccggaatttaaaaaacttgatcaccacccgaaaatctcg -gtaacc 2325

Db 151 cnccebnnhvcnvhbnnhrwayrhddardd 183  
| : ::| : : :| : ::| : : :  
Cp 2324 cgaacgcccaccctcaagaactactatagcgt 2292

RESULT 6  
ID V44650 standard; DNA; 91 BP.  
AC V44650;  
DT 06-OCT-1998 (first entry)  
DE Mammalian DNA replication origin consensus sequence; unloresconsensus.  
KW DNA replication origin; human; mammal; unloresconsensus;  
KW anti-gene; DNA replication inhibitor; shuttle vector construct creation  
KW gene therapy; ss.

OS  
PN  
PD  
PE  
PR  
PR  
PA  
PI  
WPI

MANUEL, I.D.  
WO9827200-A2.  
12-JUN-1998.  
12-DEC-1997; CA0972.  
21-MAY-1997; US-0473322.  
16-DEC-1996; US-033374.  
(VMC-) UNIV MCILL.  
COSCONS NH, Nielsen TO, Price GB, Zannits-Hadjopoulos M  
WPI: 98-3627700/11.

PT Human or mammalian origin of replication consensus sequences - for  
PT inhibiting DNA replication, for controlling initiation of  
PT replication, maintaining circular plasmids and in assembly of human  
PT artificial chromosomes  
PS Claim 1, Page 42, 54pp, English.

in its sequence represents a human or mammalian DNA replication origin. The consensus sequences of the invention, designated uniorconsensus. CC Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication CC in vivo or in vitro. The consensus sequences can also be inserted into an CC expression vector, used subsequently for in vitro transfection of CC mammalian cells, to control initiation of DNA replication. They can also

CC be used to maintain circular plasmids that are capable of  
CC semi-conservative replication in proliferating mammalian cells, or  
CC inserted into mammalian or human artificial chromosome vectors for gene  
CC therapy. Particularly, they are used to create shuttle vector constructs  
CC for defining the essential mammalian elements required for maintenance of  
CC chromosomal function. The consensus sequence can be combined with cloned  
CC human telomeres and large centromeric blocks for assembly of human  
CC artificial chromosomes and maintained as bacterial plasmids, circular or  
CC linear, large or small yeast artificial chromosomes (YACs) or as episomal  
CC elements.

Query Match	1.28;	Score 33;	DB 46;	Length 91;
Best Local Similarity	10.88;	Pred. No. 2.82e-04;		
Matches	9;	Conservative	49;	Mismatches 25; Indels 0; Gaps 0;

[illegible]

RESULT	7
ID	V44650 standard; DNA; 91 BP

AC	06-OCT-1998 (first entry)	
DT	Mammalian DNA replication origin consensus sequence, uniorsconsensus.	
DE	DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus;	
KW		

KW	anti-gene; DNA replication inhibitor; shuttle vector construct creation,
RV	gene therapy; ss.
OS	Mammalia.
PN	MO9827200-A2.
PD	23-JUN-1998.
PF	12-DEC-1997; CA0972.
PR	21-MAY-1997; US-047322.
PA	16-DEC-1996; US-033374.
PI	(UYMC-) UNIV MCGILL.
DR	Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos M; WPI: 98-362770/31.
PT	Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human artificial chromosomes
PS	Claim 1: Page 42; 54pp: English.
CC	This sequence represents a human or mammalian DNA replication origin consensus sequences of the invention, designated unlotconsensus. Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned human telomeres and large centromeric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or linear, large or small yeast artificial chromosomes (YACs) or as episomal elements.
SQ	Sequence    91 BP;    15 A;    1 C;    4 G;    7 T;
Query Match	1.2%; Score 34; DR 46; Length 91;
Best Local Similarity	11.5%; Pred. No. 8.68e-05;
Matches	9; Conservative 47; Mismatches 22; Indels 0; Gaps 0;
Dc	11 www.kdnavvgsakrwwkwhrassacmdwkaaktkgkwgwarrywqkrmwtkwkw 70
Cp	157 tgaatcatattgtaattgttgtagggcggtgatatttttggtaatatagcaacaa 98
Dd	71 sdatakwwwkdakwkmvr 88
Cp	97 gtatgtatgttgtaacaa 80
RESULT	8
ID	Q70467 standard: DNA; 114 BP.
AC	Q70467; .
DT	05-APR-1995 (first entry)
KM	Genetic DNA sequence to generate a random TSAR peptide library.
KW	TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW	effector domain; concatenated heterofunctional protein; linker;
KW	direct; rapid; detection; screening; treatment; generic; ss.
OS	Synthetic.
FH	Key
FT	misc_feature
FT	Location/Qualifiers
FT	55..60
FT	/tag= a
FT	/note= "this sequence represents 'Z'; Z can be a
FT	sequence of 6, g or 12 nucleotides (see
FT	comments)"
PN	MO9418318-A.
PD	18-AUG-1994.
PF	01-FEB-1994; U00977.
PR	01-FEB-1993; US-013416.
PR	30-DEC-1993; US-176500.
PR	31-JAN-1994; US-189331.
PA	(UYNC-) UNIV NORTH CAROLINA.
PI	Fowlkes DM, Kay BK;
DR	WPI: 94-279739/34.
OR	P-PSDB; R65153.

[illegible]





